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RESULT 5
AAW31706
ID   AAW31706 standard; protein; 1363 AA.
XX
AC   AAW31706;
XX
DT   15-JUN-2007  (revised)
DT   25-MAR-2003  (revised)
DT   14-APR-1998  (first entry)
XX
DE   Bovine coronavirus E2 (S) protein.
XX
KW   BCV; E2 protein; peplomer protein; S spike; antigen; vaccine; cattle;
KW   BOND_PC; S peplomer polypeptide precursor;
KW   S peplomer polypeptide precursor (Bovine coronavirus);
KW   spike glycoprotein; spike glycoprotein (bovine coronavirus); G05529;
KW   G06944; G09405; G016020; G016021; G019051; G019061; G019064; G046789;
KW   G046813.
XX
OS   Bovine coronavirus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .17
FT                   /label= Sig_peptide
FT   Protein         18. .1363
FT                   /label= Mat_protein
FT   Domain          1306. .1338
FT                   /note= "transmembrane domain"
XX
PN   US5672355-A.
XX
PD   30-SEP-1997.
XX
PF   22-DEC-1993;   93US-00171763.
XX
PR   22-AUG-1989;   89US-00397689.
PR   18-OCT-1991;   91US-00779500.
PR   19-DEC-1991;   91US-00811422.
XX
PA   (VETE-) VETERINARY INFECTIOUS DISEASE.
XX
PI   Babiuk LA,  Parker MD,  Cox GJ;
XX
DR   WPI; 1997-488823/45.
DR   N-PSDB; AAT89387.
DR   PC:NCBI; gi17529675.
DR   PC:SWISSPROT; P25190.
XX
PT   Vaccines against bovine coronavirus - containing recombinant bovine
PT   coronavirus polypeptide(s).
XX
PS   Claim 13; Fig 3; 52pp; English.
XX
CC   This polypeptide comprises the E2 protein, also designated peplomer
CC   protein or S (Spike), of bovine coronavirus (BCV). It has a mol.wt. of
CC   150 kDa exclusive of glycosylation and contains 21 potential N-linked
CC   glycosylation sites. The amino acid sequence was deduced from an clone E2
CC   cDNA (see AAT89387). The E2 gene in plasmid pT18E2 (E. coli JM105) is
CC   deposited as ATCC 68041. The BCV E3 gene (see AAT89388) is immediately 5'
CC   of the E2 gene on the viral genome and terminates 14 nucleotides upstream
CC   from the E2 initiation codon. The E2 and E3 genes have been cloned and
CC   can be used for the recombinant production of BCV polypeptides, using
CC   e.g. Spodoptera frugiperda Sf9 insect cells as host cells. Glycosylated
CC   and non-glycosylated recombinant E2 and E3 (see AAW31707) are useful as
CC   components of vaccines directed toward preventing BCV infection, or
CC   reducing the severity of BCV infection, in bovine populations. (Updated
CC   on 25-MAR-2003 to correct PF field.)
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CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 1363 AA;

Query Match 95.2%; Score 6965; DB 2; Length 1363;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1300; Conservative 25; Mismatches 38; Indels 9; Gaps 0;

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Qy          1 MFLILLISLPNAFAVIGDLKCTTVSINDVDTGAPSISTDVVDVTNGLGTYYVLDRVYLNT 60
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db          1 MFLILLISLPNAFAVIGDLKCTTVSINDVDTGAPSISTDIVDVTNGLGTYYVLDRVYLNT 60

Qy         61 TLLLNGYYPTSGSTYRNMALKGTLLLSTLNFKPPFLSDFIDGVFAKVKNTKVIKDGVMYS 120
              |||||||||||||||||||||||||||| ||||||||||||:|:|||||||||||| |||||
Db         61 TLLLNGYYPTSGSTYRNMALNGTLLLSRLNFKPPFLSDFINGIFAKVKNTKVIKNGVMYS 120

Qy        121 EFPAITIGSTFVNTSYSVVVQPHTTNLDNKLQGLLEISVCQYTMCDYPHTMCHPNLGNKR 180
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Db        121 EFPAITIGSTFVNTSYSVVVQPHTTNLDNKLQGLLEISVCQYTMCEYPHTICHPKLGNKR 180

Qy        181 IELNHWDTGVVPCLYKRNFTYDVNADYLYSHFYQEGGTFYAYFTDTGVVTKFLFHVYLGT 240
              |:|||||||||| |||||||||||||||| ||||||||||||||||||||||:|||||
Db        181 VELNHWDTGVVSCLYKRNFTYDVNADYLYFHFYQEGGIFYAYFTDTGVVTKFLFNVYLGT 240

Qy        241 VLSHYYVMPLTCNSAMTLEYWVTPLTFKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLS 300
              |||||||:|||:|||||||||||| ||||||||||||||||||||||||||||||||||||
Db        241 VLSHYYVLPLTCSSAMTLEYWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLS 300

Qy        301 IAPSTGVYELNGYTVQPIADVYRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSNCNFNM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IAPSTGVYELNGYTVQPIADVYRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSNCNFNM 360

Qy        361 SSLNSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQMGNLGYLQSFNYRI 420
              |||||||||||||||||||||||| ||||||||||||||:|||||||||||||
Db        361 SSLNSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRI 420

Qy        421 DTTATSCQLYYNLPAANVSISRFNPSIWNRRFGFTEQSVFKPQPVGVFTQHDVVYAQHCF 480
              |||||||||||||:|||:|||||| ||||||||| ||||||||| ||||||||||
Db        421 DTTATSCQLYYNLPAANVSVSRFNPSIWNRRFGFTEQFVFKPQPVGVFTHHDVVYAQHCF 480

Qy        481 KAPTNFCPCKLNGSLCVGSGFGIDAGYKNSGIGTCPAGTNYLTCYNAMQCDCLCTPDPIL 540
              ||| |||||||:|||||:| ||||||||||||||||||||||:|| ||||||||||
Db        481 KAPKNFCPCKLDGSLCVGNGPGIDAGYKNSGIGTCPAGTNYLTCHNAAQCDCLCTPDPII 540

Qy        541 SNSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPQAFLGWSVDSCLQGDRCNI 600
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        541 SNSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPQAFLGWSVDSCLQGDRCNI 600

Qy        601 FANFILHGVNSGTTCSTDLQKSNTDIILGVCVNYDLYGITGQGIFVEVNAIYYNSWQNLL 660
              ||||| | ||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        601 FANFIFHDVNSGTTCSTDLQKSNTDIILGVCVNYDLYGITGQGIFVEVNAIYYNSWQNLL 660

Qy        661 YDSNGNLYGFRDYLINRTFMIRSCYSGRVSAGFHSNSSEPALLFRNIKCNYVFNNTLSRQ 720
              |||||||||||||||||||||||||||||| ||:||||||||||||||||||||||||||
Db        661 YDSNGNLYGFRDYLINRTFMIRSCYSGRVSAAFHANSSEPALLFRNIKCNYVFNNTLSRQ 720

Qy        721 LQPINYFDSYLGCVVNADNSISSSVQTCDLIVGSGYWGDYSTQRRSRRTITTGYRFTNFE 780
              |||||||||||||||||||||||| ||||||||||  ||||:|||||| ||||||||||||
Db        721 LQPINYFDSYLGCVVNADNSISSVVQTCDLIVGSGYCVDYSTKRRSRRAIITGYRFTNFE 780

Qy        781 PFTVNPVNDSLHPVGGLYEIQIPSEFTIGNMEEFIQTRSPNVTIDCPVFVCGDYAACNSQ 840
              ||||| ||||| |||||||||||||||||||||||| |||||||  ||||||||||||
Db        781 PFTVNSVNDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPNVTIDCSAFVCGDYAACNSQ 840

Qy        841 LVEYGSFCDNINAILIEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDDINFSPVL 900
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        841 LVEYGSFCDNINAILIEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDDINFSPVL 900
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Qy        901 GCLGSECNKVSSRSAIEDLLFSKVKLSDVGFVDAYNNCTGGAEIRDLICVQSYNGIKVLP 960
              ||||| |||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        901 GCLGSACNKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYNGIKVLP 960

Qy        961 PLLSENQISGYTLAATFASLFPPWSAAAGVPFYLNVQYRINGIGVTMDVLTQNQKLISNA 1020
              |||| |||||||||||| ||||||| ||| ||||||||||||||||||||||:|||||||:||
Db        961 PLLSVNQISGVTLAATSASLFPPLSAAVGVPFYLNVQYRINGIGVTMDVLSQNQKLIANA 1020

Qy       1021 FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNKFGAISASLQEILSRLDA 1080
              ||||||||||||||||||||||||||||||||||||||||||||:||||||:||||||||||
Db       1021 FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRLDA 1080

Qy       1081 LEAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINFCGNG 1140
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1081 LEAQAQIDRLINGRLTALNVYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINFCGNG 1140

Qy       1141 NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTNMFT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTNMFT 1200

Qy       1201 GSGYYYPEPITGNNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPD 1260
              |||||||||||||||||||||||||||||||||||||| ||||||||||||| :|||
Db       1201 GSGVYYPEPITGNNVVVMSTCAVNYIKAPDVMLNISTPNLHDFKEELDQWFKNQTSVAPD 1260

Qy       1261 LSLDYINVTFLDLQDEMNRLQEAIKVLNHSYINLKDIGTYEYYVKWPWYVWLLIGLAGVA 1320
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||| ||||
Db       1261 LSLDYINVTFLDLQDEMNRLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320

Qy       1321 MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD 1363
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Db       1321 MLVLLFFICCCTGCGTSCFKICGGCCDDYTGHQELVIKTSHDD 1363
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